RAW SEQUENCE HISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/747, 029Source: 0/PEDate Processed by STIC: 4/6/200/

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

SERIAL NUMBER: ()9

ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". The amino acid number/text at the end of each line "wrapped" down to the next line. Wrapped Aminos This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces. The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs Misaligned Amino Acid Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers. Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed. Sequence(s) _____ contain n's or Xaa's which represented more than one residue. Variable Length As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. Patentin ver. 2.0 "bug" A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. **Skipped Sequences** missing. If intentional, please use the following format for each skipped sequence: Sequence(s) (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). Skipped Sequences missing. If intentional, please use the following format for each skipped sequence. Sequence(s) _ (NEW RULES) <210> sequence id number <400> sequence id number 000 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing. (NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. (NEW RULES) Valid response is Artificial Sequence. Use of <220>Feature Sequence(s) ____ are missing the <220>Feature and associated headings. (NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted Patentin ver. 2.0 "bug" file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biolechnology Systems Branch - 4/06/2001

OIPE

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Input Set : A:\PTO.txt
                                                                                  Does Not Comply
                     Output Set: N:\CRF3\04162001\1747029.raw
                                                                             Corrected Diskette Needed
      3 <110> APPLICANT: Union, Ann
              Moereels, Henri
      5
              Meheus, Lydie
      7 <120> TITLE OF INVENTION: PEPTIDES DESIGNED FOR THE DIAGNOSIS AND TREATMENT OF RHEUMATOID
              ARTHRITIS
     10 <130> FILE REFERENCE: 11362.0031NPUS00 INNS:031
     12 <140> CURRENT APPLICATION NUMBER: US 09/747,029
     13 <141> CURRENT FILING DATE: 2000-12-21
     15 <150> PRIOR APPLICATION NUMBER: EP 00870195.5
     16 <151> PRIOR FILING DATE: 2000-09-08
     18 <150> PRIOR APPLICATION NUMBER: EP 99870280.7
     19 <151> PRIOR FILING DATE: 1999-12-21
     21 <160> NUMBER OF SEQ ID NOS: 22
     23 <170> SOFTWARE: PatentIn version 3.0
     25 <210> SEQ ID NO: 1
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     26 <211> LENGTH: 18
     27 <212> TYPE: PRT
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    53 <222> LOCATION: (4)..(4)
    54 <223> OTHER INFORMATION: Xaa represents Ile, Leu, Val, Ala or Met
    57 <220> FEATURE:
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    60 <223> OTHER INFORMATION: Xaa represents His, Lys, Arg, Asp, Glu, Ser, Thr, Tyr, Phe or Trp
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    66 <223> OTHER INFORMATION: Xaa represents Gly
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DATE: 04/16/2001

TIME: 17:23:51

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/747.029

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RAW SEQUENCE LISTING
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                     PATENT APPLICATION: US/09/747,029
                                                            TIME: 17:23:51
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                     Output Set: N:\CRF3\04162001\1747029.raw
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     83 <222> LOCATION: (10)..(10)
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     89 <222> LOCATION: (11)..(11)
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     114 <223> OTHER INFORMATION: Xaa represent Arg, Lys, His, Asp, Glu, Ser, Thr, Gln, Asn, Tyr, P
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     121 <223> OTHER INFORMATION: Xaa represents Gly
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     127 <223> OTHER INFORMATION: Xaa represents Tyr, His, Lys, Arg, Asp, Glu, Ser, Thr, Gln, Asn,
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     140 <211> LENGTH: 15
    141 <212> TYPE: PRT
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PATENT APPLICATION: US/09/747,029
                                                         TIME: 17:23:51
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207 <220> FEATURE:
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209 <222> LOCATION: (12)..(12)
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217 <223> OTHER INFORMATION: Xaa represents Gly
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DATE: 04/16/2001

RAW SEQUENCE LISTING

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                                                              TIME: 17:23:51
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                     Output Set: N:\CRF3\04162001\1747029.raw
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     221 <221> NAME/KEY: MOD_RES
     222 <222> LOCATION: (15)..(15)
     223 <223> OTHER INFORMATION: Xaa represents Tyr, His, Lys, Arg, Asp, Glu, Ser, Thr, Gln, Asn,
               Phe or Trp
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DATE: 04/16/2001

RAW SEQUENCE LISTING

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RAW SEQUENCE LISTING
                                                              DATE: 04/16/2001
                      PATENT APPLICATION: US/09/747,029
                                                              TIME: 17:23:51
                      Input Set : A:\PTO.txt
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     303 <221> NAME/KEY: MOD_RES
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     310 <222> LOCATION: (14)..(14)
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              Phe or Trp
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                                      please correct this ever in subsequent seguenes, too
     321 <211> LENGTH: 18
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C--> 323 <213> ORGANISM: (Artificia)
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    334 <220> FEATURE:
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   361 <223> OTHER INFORMATION: Xaa represents Gly
   364 <220> FEATURE:
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields f each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 04/16/2001 PATENT APPLICATION: US/09/747,029 TIME: 17:23:52

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Output Set: N:\CRF3\04162001\I747029.raw

L:28 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1 $L\!:\!133$ M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:142 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2 $L\!:\!229$ M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 L:235 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3 L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 L:323 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4 $L\!:\!428$ M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 L:431 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 L:437 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5 $L\!:\!530~M\!:\!341~W\!:$ (46) "n" or "Xaa" used, for SEQ ID#:5 L:536 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6 L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 L:623 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7 $L\!:\!642$ M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 L:651 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8 L:664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 L:673 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9 L:692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 L:701 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10 L:720~M:341~W: (46) "n" or "Xaa" used, for SEQ ID#:10 L:729 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11 L:748 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 L:757 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12 L:776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 L:785 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13 $L\!:\!804$ M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:810 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14 L:829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 L:835 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15 $L\!:\!854$ M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 L:860 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16 $L:873\ M:341\ W:$ (46) "n" or "Xaa" used, for SEQ ID#:16 L:879 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17 L:892 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 L:901 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18 L:914 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 L:920 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19 $L\!:\!933$ M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 L:939 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20 $L\!:\!952$ M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 L:958 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21 L:971 M:341 W: $(4\overline{6})$ "n" or "Xaa" used, for SEQ ID#:21 L:977 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22 L:990 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22

• • • •